

Factor analysis of a Johne's disease risk assessment questionnaire with evaluation of factor scores and a subset of original questions as predictors of observed clinical paratuberculosis

Roy D. Berghaus^{a,*}, Jason E. Lombard^b, Ian A. Gardner^c,
Thomas B. Farver^a

^a *Department of Population Health and Reproduction, School of Veterinary Medicine,
University of California-Davis, Davis, CA 95616, USA*

^b *Centers for Epidemiology and Animal Health, U.S. Department of Agriculture, Animal and Plant Health
Inspection Service, Veterinary Services, 2150 Centre Avenue, Building B, Mail Stop 2E7,
Fort Collins, CO 80526, USA*

^c *Department of Medicine and Epidemiology, School of Veterinary Medicine,
University of California-Davis, Davis, CA 95616, USA*

Received 10 March 2005; received in revised form 8 July 2005; accepted 28 July 2005

Abstract

Factor analysis was used to examine the interrelationships among 38 variables collected as part of a Johne's disease risk assessment questionnaire completed in 2002 on 815 U.S. dairy operations. Eleven factors were extracted, accounting for two-thirds of the variance encountered in the original variables. Responses to many of the risk assessment questions were closely related. Standardized scores on the 11 factors were calculated for operations providing complete information, and were evaluated as predictors in a model-based logistic regression analysis with the outcome being whether operations had observed one or more cows with clinical signs suggestive of paratuberculosis during the previous year. A logistic regression model was also used to evaluate the predictive ability of a reduced subset of approximately one-third of the original variables that was selected to represent the derived factors. The performance of both sets of predictors was comparable with respect to goodness-of-fit and predictive ability. In conclusion, the length of the current risk assessment instrument could

* Corresponding author. Tel.: +1 530 754 2159; fax: +1 530 752 5845.
E-mail address: rdberghaus@ucdavis.edu (R.D. Berghaus).

be reduced considerably without a substantial loss of information by removing or combining questions that are strongly correlated.

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Keywords: Dairy cattle; Paratuberculosis; Johne's disease; Questionnaire; Risk assessment; Factor analysis

1. Introduction

Paratuberculosis, or Johne's disease, is a chronic granulomatous enteric disease of domestic and free ranging ruminants that is caused by *Mycobacterium avium* ssp. *paratuberculosis* (MAP). Transmission of MAP is thought to occur predominately through the fecal–oral route, although other modes of transmission, such as excretion of the organisms in milk and transplacental infection, may also play important roles (Sweeney, 1996). Animals seem to be most susceptible to MAP infection shortly after birth (Larsen et al., 1975), though typically show no outward signs of disease before they are 3–5 years of age. Clinically affected cattle develop chronic diarrhea and lose weight, while animals with sub-clinical infection have decreased milk production. Compared to beef cattle, dairy cows seem to have a consistently higher estimated prevalence of the disease (Boelaert et al., 2000; Braun et al., 1990; Merkai et al., 1987; Pence et al., 2003), presumably because increased housing densities contribute to a greater level of exposure to the causative organism within infected herds. A 1996 study of dairy operations in the U.S. estimated that 21.6% of all U.S. dairies were infected with the MAP organism at a within-herd prevalence level of 10% or greater, and that as many as 40% of operations with 300 cows or more were likely to be infected, with a cost to dairy producers of over \$200 per cow in herds where $\geq 10\%$ of culled animals suffered from clinical signs of paratuberculosis (Ott et al., 1999; USDA, 1997, p. 32). Control of paratuberculosis is challenging because of the hardiness of the causative organism, the long latent period, and the inability of diagnostic methods to detect infected animals during early stages of the disease (Kennedy and Benedictus, 2001). Most current recommendations for controlling Johne's disease rely on management interventions that are designed to limit the introduction and transmission of MAP, although to a large extent these interventions have not been empirically evaluated and their use is predicated primarily on their biological plausibility (National Research Council (U.S.) Committee on Diagnosis and Control of Johne's Disease, 2003, pp. 66–68). Recently, the use of a quantitative risk assessment has been advocated for prioritizing management changes that would be most beneficial in controlling MAP infection on an individual herd basis (USDA, 2002). This process involves assigning “risk scores” to different on-farm management procedures, and may ultimately allow for a more quantitative evaluation of various management intervention strategies.

In 2002, the National Animal Health Monitoring System (NAHMS) of the U.S. Department of Agriculture (USDA) conducted a large, population-based survey of U.S. dairy operations called the Dairy 2002 study. As part of that survey, Johne's disease risk assessments were performed for 815 dairy operations to evaluate multiple management practices thought to be important in the transmission of MAP. Since many questions in the risk assessment dealt either directly or indirectly with different aspects of exposure to adult

cow manure, responses for many of the questions were interrelated, complicating interpretation of the resulting risk scores. The primary goal of the present study was to explain the complex interrelationships between the approximately three-dozen risk variables in terms of a smaller number of relatively independent, conceptually meaningful factors or latent variables. Secondly, factor scores and a subset of questions selected to represent the factors were evaluated as predictors of whether operations had observed one or more cows having clinical signs consistent with paratuberculosis during the previous 12 months.

2. Materials and methods

2.1. Study population

Sample selection methodology for the NAHMS Dairy 2002 study has been described previously (USDA, 2003, pp. 97–101). Briefly, a stratified random sample of dairy operations was selected from 21 states (California, Colorado, Florida, Idaho, Illinois, Indiana, Iowa, Kentucky, Michigan, Minnesota, Missouri, New Mexico, New York, Ohio, Pennsylvania, Tennessee, Texas, Vermont, Virginia, Washington, and Wisconsin). In January of 2002, these states accounted for approximately 85.5% of the total U.S. dairy cow population. The National Agricultural Statistics Service (NASS) developed a sampling list frame for the study based on their existing database of dairy operations, with stratification in each state based on herd size characteristics. A sample of 3876 dairies was selected for an initial screening, of which 2461 eligible operations elected to participate in the first phase of the study. Phase I consisted of the administration of a questionnaire covering general dairy management practices, and was completed between December 31, 2001 and February 12, 2002. Herds with 30 or more cows that completed the first phase of the study were subsequently invited to participate in a second phase that consisted of the administration of another questionnaire between February 25 and April 30, 2002 covering additional management and animal-health related topics. Participants in phase II of the study also had the option of having an animal health official complete a Johne's disease risk assessment for their operation. Of 1438 herds that were eligible to participate in the second phase of the study, 1013 chose to complete the additional questionnaire and 815 elected to have the Johne's disease risk assessment performed. Risk assessments were completed between March 15 and October 17, 2002.

2.2. Risk assessment questionnaire

Federal or state veterinary medical officers or animal health technicians completed the risk assessment form in conjunction with producers. Although some questions about management were answered directly by producers, animal health officials were charged with scoring most of the items based on their own subjective observations at the time of the interview. At the beginning of the interview, the following statement was read to producers by the attending animal health official, "Clinical signs of Johne's disease in cattle include chronic diarrhea and weight loss that does not respond to treatment despite a normal appetite." Producers were subsequently asked about the herd's history of Johne's disease,

including information on whether cows with clinical signs of paratuberculosis had been observed on the farm during the previous 12 months, the results of any testing for Johne's disease that had been performed during the previous 12 months, and whether the operation was currently participating in a paratuberculosis control or herd certification program. The remaining questions focused on various management conditions in five specific production areas: calving, pre-weaned calves, post-weaned heifers, bred heifers, and adult cows. Most questions (Appendix A) were directed to evaluate practices that were thought to be important in the transmission of MAP in each production area, and numerical scores were assigned to indicate the level of perceived risk, or in some cases to indicate the frequency with which a particular practice was carried out. With the exception of variables that measured the frequency of calving area observation (Q109 and Q110), or the ratio of individual calving pens to the number of adult cows (Q111), a higher score corresponded to a higher perceived risk. After risk assessments were completed, state NAHMS coordinators manually reviewed them for accuracy before sending them on to the Centers for Epidemiology and Animal Health (CEAH), where data entry and validations were completed using SAS statistical software.

2.3. Statistical analysis

An exploratory factor analysis was performed on the risk variables using SPSS statistical software (version 12.0). Extraction of the initial factors was accomplished by using the method of principal components (PC) on the correlation matrix of the original variables (Afifi et al., 2004, pp. 395–398). Determination of the number of factors to keep for interpretation was a compromise between parsimony, interpretability, and the total amount of variation in the original variables that was explained by the factors in the model. Several methods have been proposed to guide the decision of how many factors to retain, including keeping factors with an initial eigenvalue ≥ 1 (the Kaiser rule); graphing the factors against their respective eigenvalues and keeping only those that occur before the drop in the eigenvalues starts to level-off (the Scree method); and keeping the number of factors that are required to account for a given proportion of the variance observed in the original variables (Stevens, 1996, pp. 366–368). All three of these methods were considered in the current analysis. Factors were rotated to simplify their structure and enhance interpretability (Kleinbaum et al., 1988, pp. 617–622). Orthogonal and oblique factor rotations were both evaluated, but ultimately an orthogonal rotation (Varimax) was selected for the final analysis because it resulted in a relatively simple and interpretable structure while maintaining factor independence. |Factor loadings| > 0.40 were used in the interpretation of rotated factors.

Item non-response led to some missing information in the current data set, with operations that did not keep certain age groups of animals on the farm being asked to skip the corresponding sections of the questionnaire. Hence, factor analyses that both included and excluded dairies providing incomplete information were performed to evaluate the effect that this might have on the final model. Since the interpretation of factors was the same using either approach, we chose to use all available information to estimate the correlation matrix from which the initial factors were extracted. This allowed for a larger effective sample size, and seemed theoretically more appropriate than selectively

excluding the operations that raised certain age groups of animals off-site. We also evaluated herds above or below the median herd size of 130 cows separately as part of a preliminary analysis (data not shown) to determine whether the factors that would be extracted from these two groups differed substantially, but as they did not, we ultimately decided to include herds of all sizes together in the final analysis. Additionally, a separate set of recoded variables that combined what were perceived as ambiguous categories in the original variables was analyzed to evaluate the effect of possible risk score misclassification (data not shown), but interpretation of the factors that were extracted from the recoded variables was the same as that for the original variables, and so the original coding scheme was used in the final analysis.

The suitability of individual variables for use in the factor analysis was evaluated by using the Kaiser–Meyer–Olkin (KMO) measure of sampling adequacy:

$$\text{MSA}(J) = \frac{\sum_{k \neq j} r_{jk}^2}{\sum_{k \neq j} r_{jk}^2 + \sum_{k \neq j} q_{jk}^2}$$

where $\text{MSA}(J)$ is the measure of sampling adequacy for the J th variable, r_{jk} represents an element of the correlation matrix \mathbf{R} , and q_{jk} represents an element of the anti-image correlation matrix \mathbf{Q} , which is in turn defined by the equation $\mathbf{Q} = \mathbf{S}\mathbf{R}^{-1}\mathbf{S}$, where $\mathbf{S} = (\text{diag } \mathbf{R}^{-1})^{-1/2}$ (Kaiser and Rice, 1974). The MSA must lie between 0 and 1, and is described by Kaiser as a measure of the extent to which a variable “belongs to the family” of the larger group of variables, with values <0.5 being considered “unacceptable” (Kaiser, 1970).

During preliminary analysis, one of the risk variables (Q112. Are there employees on this operation who have direct contact with both pre-weaned calves and older cattle—other than at calving?) was found to have a KMO value <0.5 , suggesting that it did not fit well with the structure of the other variables, and consequently it was excluded from the final factor model. Information on herd size was not collected as part of the risk assessment form, but was available from a separate section of the survey and we chose to include it in the analysis to allow for the possibility that it may be related to several management characteristics.

After selection of a final factor model, standardized factor scores with an approximately zero mean and unit variance were calculated for herds that had provided complete information on all variables. These scores were subsequently evaluated as predictors in a model-based logistic regression analysis to determine whether they were associated with the observation of one or more cows having clinical signs that were consistent with paratuberculosis during the previous 12 months. The variable (Q112) that had been excluded from the final factor model because of a low KMO value was also evaluated in the logistic model as a possible predictor.

The functional form of continuous predictors was graphically evaluated by grouping observations into quartiles and plotting the logistic regression coefficients for the quartiles versus the group midpoints to determine whether the relationship between predictors and the outcome was approximately linear in the log odds. Different categorizations and transformations of the variables were evaluated based on these plots, and a significant change in model deviance was used as the criteria for determining the most appropriate form of the predictor.

A backward model selection procedure was used to choose the final logistic model, with P -values <0.05 being considered statistically significant. The Hosmer–Lemeshow (H–L) statistic was used to assess goodness of fit (Hosmer and Lemeshow, 2000, pp. 147–156), and the predictive ability of the model was assessed by cross-classifying the herds according to their reported outcome status and their predicted status, with a predicted probability of 0.5 being used as the cutoff. Predictive ability was further evaluated by refitting the model to a randomly selected subset of 75% of the observations, and using the resulting model to predict the probability of the outcome in the 25% of operations that were held out during model fitting. Standardized residuals, leverage values, and the change in regression coefficients resulting from the exclusion of a particular case (DF Beta values) were plotted to identify influential observations and the information provided by operations that were identified as outliers was examined to determine whether there were any apparent discrepancies or errors in the data. The extent to which the response variable may have been correlated within interviewers and states was evaluated by calculating the intra-class correlation via the *loneway* procedure in Stata version 8.0. The effect of correlated responses within interviewers was further evaluated by using Stata's *xtlogit* command to fit a population-averaged generalized estimating equation (GEE) model assuming an exchangeable correlation structure with interviewer as the grouping variable (Hosmer and Lemeshow, 2000, pp. 309–330).

Finally, a reduced subset of the original questions was selected based on the final factor model, and these variables were also evaluated as predictors in a logistic regression model to compare their predictive ability with that of the factor scores.

3. Results

Data from 815 dairy operations were included in the analysis, with risk assessments being completed by 201 different evaluators in the 21 participating states. The number of operations that provided complete information on all of the risk variables was 487, while the lowest number responding for any individual variable was 648 (see Appendix A). A plot of the eigenvalues versus the components obtained in the initial extraction of the factor analysis is shown in Fig. 1. Eleven components had an eigenvalue ≥ 1 , suggesting that 11 factors should be kept for interpretation according to the Kaiser rule, while use of the Scree method to select those factors with an eigenvalue that occurs on the down-slope of Fig. 1 would seem to suggest that 6 or 7 factors should be retained. After consideration of the amount of variance that was explained, as well as the interpretability of the resulting factors, we decided to retain 11 factors in the final model, accounting for 65% of the variance in the original 38 variables. |Factor loadings| (correlations) > 0.40 obtained for the final model are shown in Table 1, and the distribution of Pearson correlations between pairs of variables within factors is shown in Fig. 2.

A relatively simple factor structure was observed, with most variables loading high on only a single factor. There were two variables (Q301 and Q302) that loaded on both factors 5 and 6, however, indicating that they were moderately related to both. One variable related to factor 9 had a negative loading (Q111. What is the ratio of individual calving pens: adult cows?), although this was appropriate considering that its scores were inversely related to

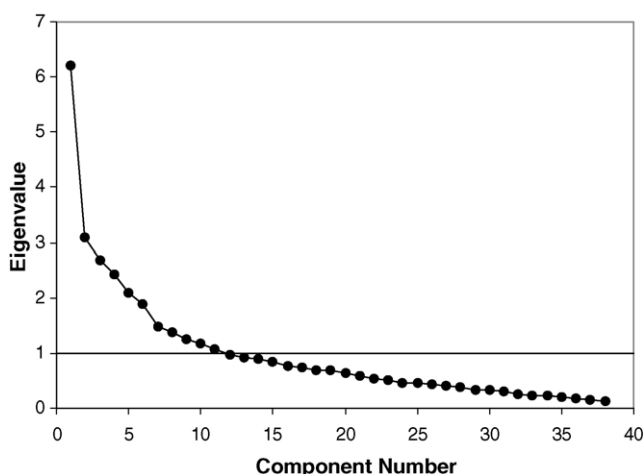


Fig. 1. Eigenvalues of 38 components extracted during factor analysis of a Johne's disease risk assessment questionnaire completed on 815 U.S. dairy operations. Factors with an eigenvalue ≥ 1 were retained in the final factor model.

those of the other variable loading high on that factor (Q101. How often is the area where cows normally calve used for more than one cow?).

Standardized factor scores were calculated for herds providing complete information on all risk variables, and these scores were subsequently evaluated as predictors in a multivariable logistic regression model, with the outcome being whether producers had or had not observed one or more cows with clinical signs that were consistent with paratuberculosis during the previous 12 months. Complete information on all risk variables and the outcome variable was available for 482 (59.1%) herds, while the remaining 333 (40.9%) herds had missing information and were consequently excluded from the logistic regression. Of the operations with missing information, 213 (64%) skipped sections of the questionnaire because certain age groups of animals were raised off-site, while the remaining 120 (36%) had incomplete data because of item non-response. Compared to the operations with complete data, those with missing information had a significantly larger median herd size (218 versus 101 cows; Mann–Whitney $P < 0.001$), and were also significantly more likely to report that they had observed one or more cows with clinical signs of paratuberculosis during the previous year (49 versus 35%; $\chi^2 = 14.4$, 1 d.f., $P < 0.001$).

For herds providing complete information, intra-class correlations were estimated to evaluate the possible effect of correlated responses within states and interviewers. Although the intra-class correlation of the outcome variable was quite low within states (ICC = 0.05), it was somewhat higher within interviewers (ICC = 0.15). Consequently, we further evaluated the effect of correlation within interviewers by comparing the estimates obtained in the final maximum-likelihood based logistic regression model to those that were obtained from a population-averaged generalized estimating equation assuming an exchangeable correlation structure within interviewers. Since the estimates obtained from the GEE were within 10% of those obtained from the original logistic regression model, however, we elected to use the simpler maximum-likelihood method for our final model.

Table 1
Sorted loadings for 11 factors extracted from 38 Johne's disease risk assessment variables evaluated during a survey of 815 U.S. dairy operations

Variables	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6	Factor 7	Factor 8	Factor 9	Factor 10	Factor 11
404. Bred heifers and cows share waterers	0.83										
405. Bred heifers and cows share feed bunks	0.83										
401. Bred heifers housed near cows	0.80										
403. Bred heifers and cows share feed, water, housing	0.74										
402. Bred heifer feed, water, housing contaminated by cow manure	0.64										
406. Bred heifers and cows share pasture	0.64										
408. Manure contamination of bred heifer feeding equipment		0.89									
308. Manure contamination of weaned calf feeding equipment		0.85									
502. Adult cow manure contamination of feed storage areas/equipment		0.81									
501. Manure contamination of cow feeders, waterers		0.48									
407. Manure spread on bred heifer pasture			0.92								
307. Manure spread on weaned calf pasture			0.91								
503. Manure spread on cow pasture			0.88								
304. Weaned calves and cows share water				0.78							
305. Weaned calves and cows share feed bunks				0.75							
303. Weaned calves and cows share feed, water, housing				0.66							
306. Weaned calves and cows share pasture				0.45							
203. Pre-weaned calves housed near cows					0.81						
204. Manure contamination of pre-weaned calf feed, water, or housing					0.73						
301. Weaned calves housed near cows				0.45	0.66						

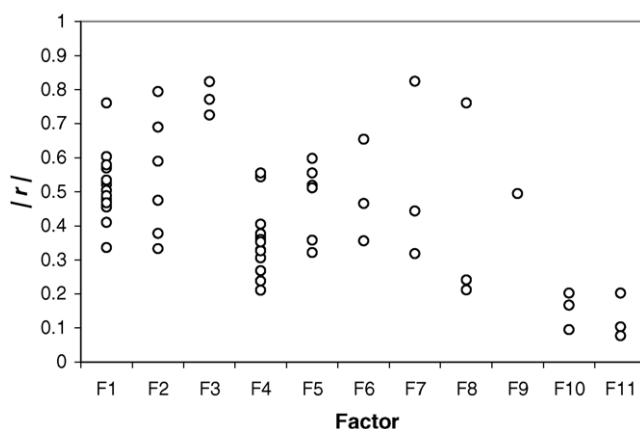


Fig. 2. Distribution of the absolute values of Pearson correlations $|r|$ between variables within each of the 11 factors extracted during factor analysis of a Johne's disease risk assessment questionnaire completed on 815 U.S. dairy operations.

Results from the final logistic regression model using the factor scores as predictors are shown in Table 2. Factors 6, 9, 10, and 11 were positively associated with observing one or more cows with clinical signs that were consistent with paratuberculosis, while factors 5, 7, and 8 were inversely related to the outcome. The deviance of the final factor score model was 538.57, and the H–L statistic was 10.41 (8 d.f.; $P = 0.237$). Using a cutoff probability of 0.5, the overall rate of correct classification was 74.4%, with 86.8% of the operations that had not observed a clinical case and 46.2% of those that had observed one or more cows with clinical signs being correctly classified. When the same model was fit to a randomly selected subset of 362 (75%) operations, the H–L statistic was 8.38 (8 d.f., $P = 0.398$) for the herds used to fit the model, and 13.09 (6 d.f., $P = 0.042$) for the operations that were held out during model estimation. The overall correct classification was 71.0% for the herds in the estimation sample and 74.2% for the validation sample. Within herds that reported no clinical cases, correct classification was 85.8% for the herds in the estimation sample and 88.6% for the held-out operations, while in herds that had observed one or more clinical cases the correct classification was 44.6 and 46.3%, respectively.

Table 2

Standardized factors associated with observing ≥ 1 cow with clinical signs of paratuberculosis during the previous 12 months in a model-based multivariable logistic regression of herds providing complete information on all variables ($n = 482$)

Variable	Coefficient	S.E.	P-value
Factor 5 (proximity of calf housing to adults)	−0.35	0.11	0.001
Factor 6 (calving area watchfulness and herd size)	0.36	0.11	0.001
Factor 7 (use of pooled milk and colostrum)	−0.37	0.11	<0.001
Factor 8 (length of time that calves are left with dams)	−0.63	0.11	<0.001
Factor 9 (group vs. individual calving pens)	0.27	0.11	0.012
Factor 10 (periparturient cow sanitation)	0.31	0.11	0.003
Factor 11 (use of the calving area as a sick pen)	0.29	0.10	0.004
Constant	−0.66	0.11	<0.001

A reduced subset of the original questions was selected based on the final factor model, with one original variable being selected to represent each factor. The variables, listed below, were selected based on consideration of their representation of the general theme of the factor, the relative strength of their factor loadings, and relevance to MAP transmission:

- Factor 1—404. Bred heifers and cows share waterers.
- Factor 2—502. Adult cow manure contamination of feed storage areas/equipment.
- Factor 3—307. Manure spread on weaned calf pasture.
- Factor 4—304. Weaned calves and cows share water.
- Factor 5—203. Pre-weaned calves housed near adults.
- Factor 6—505. Total number of cows in the herd.
- Factor 7—202a. Pasteurization of pooled milk fed to calves.
- Factor 8—107. Cows allowed to nurse calves.
- Factor 9—101. Multiple cows in the calving area.
- Factor 10—102. Extent of manure contamination in the calving area.
- Factor 11—104. Hold or treat sick cows in the calving area.

These variables were subsequently evaluated as predictors in a multivariable logistic regression model along with the previously excluded variable related to employee contact with calves and older animals (Q112) to compare their predictive ability with that of the factor scores derived from the full set of variables. The 66 bivariate correlations between these variables were all <0.3 in absolute value, with 60 (91%) of the $|\text{correlations}|$ being <0.2 , and 39 (59%) being <0.1 . The final model selected from the reduced subset of variables is shown in Table 3. Variables related to herd size and the extent of manure build-up in the calving area were positively associated with observing one or more cows with clinical signs of paratuberculosis during the previous 12 months; while variables related to the proximity of calves to adult cows, the frequency with which cows were allowed to nurse calves, and

Table 3

Variables from a reduced subset of the original questions that were associated with observing ≥ 1 cow with clinical signs of paratuberculosis during the previous 12 months in a model-based multivariable logistic regression of herds providing complete information on all variables ($n = 482$)

Variable (factor represented)	Coefficient	S.E.	P-value
203. Are pre-weaned calves housed near adult cows? (factor 5) ^a	−0.26	0.11	0.024
505. Herd size category (factor 6)			<0.001
<100 cows	Referent	Referent	Referent
100–499 cows	0.65	0.23	0.005
>500 cows	1.38	0.32	<0.001
202a. Is pooled milk that is fed to calves pasteurized? (factor 7)			<0.001
Do not feed pooled milk	Referent	Referent	Referent
Yes	−0.28	0.56	0.619
No	−0.87	0.22	<0.001
107. How often are cows allowed to nurse calves? (factor 8) ^a	−0.30	0.11	0.006
102. Extent of manure build-up in the calving area (factor 10) ^a	0.26	0.11	0.015
Constant	−0.63	0.19	0.001

^a Variables have been standardized so that coefficients represent the effect of a 1 S.D. change in the predictor.

whether pooled milk fed to calves was pasteurized, were inversely related to the outcome. The deviance of the final reduced subset model was 554.66, and the H–L statistic was 8.59 (8 d.f., $P = 0.378$). The overall rate of correct classification was 72.6%, with 87.8% of the operations that had not observed a clinical case and 45.0% of those that had observed one or more cows with clinical signs being correctly classified. When the same model was fit to a randomly selected subset of 362 (75%) operations, the H–L statistic was 2.25 (8 d.f., $P = 0.973$) for the herds used to fit the model and 12.61 (6 d.f., $P = 0.050$) for the operations that were held out during model selection. The overall correct classification was 71.5% for the herds in the estimation sample and 72.5% for the validation sample. Within herds that reported observing no clinical cases, correct classification was 84.1% for the herds used in the estimation sample and 86.1% for the held-out operations, while in herds that had observed one or more clinical cases the correct classification was 42.3 and 46.3%, respectively.

4. Discussion

In the current study, information collected on 38 Johne's disease risk assessment variables was evaluated using an exploratory factor analysis, resulting in the retention of 11 factors that accounted for two-thirds of the variance observed in the original data. The distribution of correlations between variables within factors demonstrates their degree of inter-relatedness, with the highest correlations belonging to those variable pairs that have the highest factor loadings. The analysis supports the supposition that many of the items evaluated in the risk assessment were strongly correlated, and that while information was collected on more than three-dozen risk variables, the number of independent constructs that were measured by the instrument seems to be much smaller. Our subjective interpretation of what the factors in the final model represent is outlined below:

- Factor 1—Commingle of bred heifers and adults.
- Factor 2—Shared equipment for feed and manure handling.
- Factor 3—Manure spread on pastures.
- Factor 4—Commingle of weaned calves and adults.
- Factor 5—Proximity of calf housing to adults.
- Factor 6—Calving area watchfulness and herd size.
- Factor 7—Use of pooled milk and colostrum.
- Factor 8—Length of time that calves are left with dams.
- Factor 9—Group versus individual calving areas.
- Factor 10—Periparturient cow sanitation.
- Factor 11—Use of the calving area as a sick pen.

Because of the subjective nature of factor analysis, it is important to recognize that other interpretations of the latent variables are possible and may be equally valid. Nonetheless, the analysis does provide insight into the way that these management practices tend to cluster together on farms, and the structure of factors was not dependent on the coding of risk scores, the type of rotation that was used, or the manner in which missing data were handled. One of the main advantages of using factor analysis in this study was its ability to

identify groups of closely related variables from among the larger group of 38 risk assessment questions. This is a task that could not have been readily accomplished by examining the matrix of 703 bivariate correlations.

In the logistic regression analysis, factor scores and a reduced subset of the original variables selected based on the factor model were evaluated as predictors of whether operations had observed one or more cows with clinical signs that were consistent with paratuberculosis during the previous year. This is an admittedly subjective outcome and may be prone to misclassification, with some producers reporting uninfected cows that they believed met the stated case description, and others failing to recognize or remember animals with clinical disease. Although the use of testing results would have offered a less subjective outcome, only 285 (35.0%) operations had performed any type of testing during the previous year, and follow-up testing conducted during the Dairy 2002 study was limited to 94 (11.5%) of the 815 herds. Conversely, information on whether producers had observed cows with clinical signs that were consistent with paratuberculosis was available for 803 (98.5%) operations.

Factor scores were only calculated for herds providing complete information because calculation for herds with missing information would have required the imputation of risk variable scores. As a result, herds with missing information were excluded from the logistic regression analysis and this may have biased the results. These herds were different from those providing complete information in that they had a significantly larger median herd size, and they were more likely to have reported observing one or more clinical cases of paratuberculosis during the previous year. Consequently, it is important to recognize that the associations observed in the logistic regression analysis may not apply to the herds with missing data, many of which were excluded because they raised one or more age groups of animals off-site.

In the logistic regression model using factor scores as predictors, standardized risk scores for factors 6, 9, 10, and 11 were significantly higher in herds that had observed cows with clinical signs of paratuberculosis, suggesting that these herds were larger, more likely to use group calving areas, less attentive to sanitation in areas used by periparturient cows, and more likely to keep sick cows in the calving area. Conversely, scores for factors 5, 7, and 8 were significantly lower in herds observing cows with clinical signs of paratuberculosis, indicating that these herds had a lower perceived risk in terms of the proximity of calves to adult cows, the use of pooled colostrum and milk, and the length of time that calves were left with their dams after birth. In the analysis using the reduced subset of original variables, large herd size and contamination of the calving area with manure (variables representing factors 6 and 10) were positive predictors of the observation of clinical cases, while clinical disease was less likely to be reported in herds that housed pre-weaned calves near adult cattle (factor 5), fed unpasteurized pooled milk (factor 7), and those that frequently allowed cows to nurse calves after birth (factor 8).

Although some of the inverse associations that were observed in the logistic regression analysis may seem paradoxical for management practices that would be expected to increase risk, it is important to recognize that the cross-sectional design of the study does not allow differentiation between management practices that are risk factors for clinical disease and those that might have been implemented in response to disease. For example, a previous report based on data from the USDA's Dairy '96 study noted that larger herds and

those that used group calving areas were more likely to be classified as MAP infected, while herds with a previous history of paratuberculosis were more likely to remove calves from their dams immediately after birth (Wells and Wagner, 2000). Though several of the factors and individual variables that we evaluated were not significantly associated with the observation of cows having clinical signs of paratuberculosis, this does not necessarily imply that they are not important in the transmission of MAP. Factors associated with the observation of clinical cases may be quite different from those associated with the prevalence of infection. On many operations, infected animals are likely to be removed from the herd before they have an opportunity to progress to clinical disease as a result of culling for decreased milk production, mastitis, infertility, or other problems.

The fit of the logistic regression models using the factor scores and the reduced subset of original variables as predictors was comparable as measured by the H–L goodness-of-fit statistic. On cross-validation, both sets of predictors produced models that seemed to fit reasonably well for the estimation samples, although both demonstrated a lack of fit in the observations that were held out during model fitting. This may have been due in part to the relatively small sample size ($n = 120$) for the group of held-out observations, which resulted in low expected counts (<5) for at least two cells in the tables used to calculate the H–L statistic, even when the tables were limited to six groups. Predictive abilities of the models were also similar, with both yielding overall correct classification percentages of 71–74%. As would be expected, the proportion of correct classifications was consistently higher for the herds that had not observed any clinical cases because this was the more prevalent group. On cross-validation, both sets of predictors had a slightly higher percentage of correct classifications in the validation sample than in the estimation sample, which was likely just a reflection of random differences in the distribution of predicted probabilities in the two groups of operations.

Information collected during the risk assessment may have been affected by the subjectivity of many of the questions/observations, and with over 200 different evaluators, the variation in scoring may have influenced the outcome of the model. A workshop and CD presentation were used to educate the over 200 evaluators prior to the study. Although risk assessments were completed over a 7-month period, observations made by the evaluators may not have been ‘typical’ representations of the operations due to the timing of the evaluations and influences such as weather, fieldwork, etc. An evaluation of inter-observer reliability for a similar questionnaire was conducted in Pennsylvania where six veterinarians experienced in working with MAP infected operations each performed risk assessments on the same five dairies. Results from this small study suggested that although the scoring of individual questions was variable, with some evaluators tending to assign higher or lower scores, identification of the highest-risk management areas for each of the farms was consistent (Hutchinson et al., Veterinary Science Dept., Pennsylvania State University, Unpublished data). In the current study, we used a generalized estimating equation approach to assess the effect that intra-interviewer correlation may have had on the logistic regression model, but since the adjusted estimates were not meaningfully different from the unadjusted, we chose to use the simpler maximum-likelihood model.

Although sampling for the Dairy 2002 study was implemented using stratification based on herd size, we are not aware of any commercially available software that will allow the

incorporation of complex survey characteristics when conducting a factor analysis. Consequently, the relationships that were observed in the current sample of farms, which contained a greater proportion of large (i.e. >500 cows) dairies to ensure that such operations would be adequately represented, may differ from those of the overall dairy population (Skinner et al., 1986), though it is not straightforward to predict in what ways the population relationships may differ. The logistic regression analyses relating factor scores and individual variables to the observation of cows with clinical signs of disease were also conducted using a model-based, rather than a sampling design-based approach, since they were performed as a secondary extension of the factor analysis.

5. Conclusions

Exploratory factor analysis demonstrated that many of the variables included in a Johne's disease risk assessment questionnaire that was administered as part of the NAHMS Dairy 2002 study were closely related. Factor scores and a reduced subset of approximately one-third of the original variables were both evaluated as predictors of whether operations had observed one or more cows with clinical signs that were consistent with paratuberculosis during the previous year. The performance of both sets of predictors was comparable with respect to goodness-of-fit and predictive ability, suggesting that the length of the current risk assessment instrument could be reduced considerably without a substantial loss of information by removing or combining questions that are strongly correlated. If the goal of the instrument is to educate producers rather than to collect information, then there may be an added benefit to asking questions that re-emphasize the importance of particular management practices across a number of different production areas.

Acknowledgement

Supported in part by an Austin Eugene Lyons Fellowship, University of California-Davis.

Appendix A. Questions included in the Johne's disease risk assessment administered as part of the NAHMS Dairy 2002 survey

	Range of scores (median)	<i>n</i>	Mean (S.D.)
A. Calving area			
101. How often is the area where cows normally calve used for more than one cow?	0–10 (10.0) 0 = never, 10 = always	815	6.9 (3.7)
102. What is the extent of manure build-up in the area where cows normally calve?	0–10 (5.0) 0 = none, 10 = extensive	810	4.9 (3.0)
103. How often are calves born in areas other than where cows normally calve?	0–10 (3.0) 0 = never, 10 = occurs ≥ 5 out of 10 calvings	814	3.4 (2.7)

Appendix A. (Continued)

	Range of scores (median)	<i>n</i>	Mean (S.D.)
104. How often is the area where cows normally calve also used for holding or treating sick cows?	0–10 (0.0) 0 = never, 10 = always	814	2.1 (2.8)
105. How often are cows clinically ill with JD or suspected of having JD kept in areas where cows normally calve?	0–10 (0.0) 0 = never, 10 = always	811	0.8 (2.2)
106. How often do newborn calves stay with their dams for more than 3 h after they are born?	0–10 (5.0) 0 = never, 10 = always	814	5.6 (3.4)
107. How often are cows allowed to nurse calves?	0–10 (5.0) 0 = never, 10 = always	815	5.0 (3.7)
108. What is the extent of manure on a majority of cows' udders in the calving area?	0–10 (3.0) 0 = none, 10 = udders caked with manure	811	2.4 (1.6)
109. On average, how many times is the calving area observed daily between 6 a.m. and 6 p.m.?	1–5 (4.0) 1 = 0–1 times, 5 = ≥ 12 times	801	3.6 (1.0)
110. On average, how many times is the calving area observed daily between 6 p.m. and 6 a.m.?	1–5 (2.0) 1 = 0–1 times, 5 = ≥ 12 times	805	2.5 (1.2)
111. What is the ratio of individual calving pens: adult cows?	1–4 (2.0) 1 = no individual pens, 4 = ≥ 1 pen per 25 cows	812	1.8 (0.9)
112. Are there employees on this operation who have direct contact with both pre-weaned calves and older cattle (other than at calving)?	1–2 (2.0) 1 = no, 2 = yes	809	1.8 (0.4)
B. Pre-weaned calves			
201. How often is pooled colostrum fed to calves?	0–10 (0.0) 0 = never, 10 = always	714	3.3 (3.9)
201a. What is the source of colostrum fed to calves?	1–3 (2.0) 1 = test negative cows, 2 = unknown status cows, 3 = test positive cows	648	1.9 (0.3)
202. How often is pooled milk fed to calves?	0–10 (5.0) 0 = never, 10 = always	714	4.8 (4.5)
202a. Is pooled milk that is fed to calves pasteurized?	0–3 (3.0) 0 = do not feed pooled milk, 1 = yes, 3 = no	702	1.7 (1.5)
203. Are pre-weaned calves housed near adult cows?	0–10 (0.0) 0 = never, 10 = always	714	2.4 (3.6)
204. Adult cow manure contamination of the milk, feed, water, or housing area of pre-weaned calves	0–10 (0.0) 0 = none, 10 = extensive	714	1.1 (2.0)

Appendix A. (Continued)

	Range of scores (median)	<i>n</i>	Mean (S.D.)
C. Post-weaned heifers			
301. Are post-weaned calves housed near adult cows?	0–10 (0.0) 0 = never, 10 = always	690	2.8 (3.7)
302. Adult cow manure contamination of the feed, water, or housing area of post-weaned heifers	0–5 (0.0) 0 = none, 5 = extensive	690	0.6 (1.1)
303. How often do post-weaned heifers share feed (including left-over feed—weighbacks), water, or housing with adult cows?	0–5 (0.0) 0 = never, 5 = always	690	1.1 (1.8)
304. Are waterers shared between post-weaned heifers and adult cows?	1–2 (1.0) 1 = no, 2 = yes	688	1.1 (0.3)
305. Is feed bunk space shared between post-weaned heifers and adult cows?	1–2 (1.0) 1 = no, 2 = yes	685	1.1 (0.3)
306. How often do post-weaned heifers share pasture with adult cows?	0–5 (0.0) 0 = never, 5 = always	688	0.5 (1.2)
307. How often during the growing season is manure spread on forage ground that is either grazed by post-weaned heifers or harvested and fed to post-weaned heifers?	0–5 (0.0) 0 = never, 5 = always	687	1.0 (1.4)
308. Manure contamination of equipment used to feed post-weaned heifers	0–5 (0.0) 0 = none, 5 = extensive	689	0.6 (0.9)
D. Bred heifers			
401. Are bred heifers housed near adult cows?	0–4 (3.0) 0 = never, 4 = always	675	2.4 (1.7)
402. Adult cow manure contamination of the feed, water, or housing area of bred heifers	0–4 (1.0) 0 = none, 4 = extensive	677	1.2 (1.3)
403. How often do bred heifers share feed (including left-over feed—weighbacks), water, or housing with adults?	0–4 (2.0) 0 = never, 4 = always	676	2.2 (1.7)
404. Are waterers shared between bred heifers and adults?	1–2 (2.0) 1 = no, 2 = yes	670	1.5 (0.5)
405. Is feed bunk space shared between bred heifers and adults?	1–2 (1.0) 1 = no, 2 = yes	657	1.5 (0.5)
406. How often do bred heifers share pasture with adult cows?	0–4 (0.0) 0 = never, 4 = always	676	1.4 (1.7)
407. How often during the growing season is manure spread on forage ground that is either grazed by bred heifers or harvested and fed to bred heifers?	0–4 (0.0) 0 = never, 4 = always	676	1.1 (1.3)

Appendix A. (Continued)

	Range of scores (median)	<i>n</i>	Mean (S.D.)
408. Manure contamination of equipment used to feed bred heifers	0–4 (0.0) 0 = none, 4 = extensive	677	0.6 (0.9)
E. Adult cows			
501. Adult cow manure contamination of feeders or waterers	0–4 (1.0) 0 = none, 4 = extensive	815	1.1 (0.8)
502. Adult cow manure contamination of feed storage areas or feeding equipment	0–4 (0.0) 0 = none, 4 = extensive	814	0.7 (0.8)
503. How often during the growing season is manure spread on forage ground that is either grazed by adult cows or harvested and fed to adult cows?	0–4 (1.0) 0 = never, 4 = always	812	1.2 (1.3)
504. How often do adult cows have access to manure storage areas?	0–4 (0.0) 0 = never, 4 = always	814	0.6 (1.2)
505. How many dairy cows, whether dry or in milk, were on this operation on January 1, 2002?	17–8326 (130)	815	417 (756)

Note: summary statistics reflect the response of sampled herds rather than population estimates (*n* = number of responding operations; S.D. = standard deviation).

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